OIPE

Hi

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/837,446

DATE: 05/07/2001
TIME: 17:55:04

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05072001\I837446.raw

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 4 <110> APPLICANT: Butcher, Eugene C.
 5        Campbell, James J.
 6        Rottman, James B.
 7        Wu, Lijan
 9 <120> TITLE OF INVENTION: Modulation of Systemic Memory T Cell
10        Trafficking
12 <130> FILE REFERENCE: STAN-110CON
14 <140> CURRENT APPLICATION NUMBER: US/09/837,446
15 <141> CURRENT FILING DATE: 2001-04-17
17 <150> PRIOR APPLICATION NUMBER: 09/232,878
18 <151> PRIOR FILING DATE: 1999-01-15
20 <160> NUMBER OF SEQ ID NOS: 6
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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25 <211> LENGTH: 1677
26 <212> TYPE: DNA
27 <213> ORGANISM: H. sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (183)...(1265)
32 <223> OTHER INFORMATION: CCR4, Chemokine receptor coding sequence
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36 tctctcattt cccttctcct tctccctcag tctccacatt caacattgac aagtccattc     120
37 agaaaagcaa gctgcttctg gttgggccca gacctgcctt gaggagcctg tagagttaaa     180
38 aa`atg aac ccc acg gat ata gca gat acc acc ctc gat gaa agc ata         227
39     Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile
40     1               5                  10                  15
42 tac agc aat tac tat ctg tat gaa agt atc ccc aag cct tgc acc aaa        275
43 Tyr Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys
44                  20                  25                  30
46 gaa ggc atc aag gca ttt ggg gag ctc ttc ctg ccc cca ctg tat tcc       323
47 Glu Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser
48                  35                  40                  45
50 ttg gtt ttt gta ttt ggt ctg ctt gga aat tct gtg gtg gtt ctg gtc       371
51 Leu Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val
52                  50                  55                  60
54 ctg ttc aaa tac aag cgg ctc agg tcc atg act gat gtg tac ctg ctc       419
55 Leu Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu
56         65                  70                  75
58 aac ctt gcc atc tcg gat ctg ctc ttc gtg ttt tcc ctc cct ttt tgg       467
59 Asn Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp
60 80                  85                  90                  95
62 ggc tac tat gca gca gac cag tgg gtt ttt ggg cta ggt ctg tgc aag       515
63 Gly Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys
64                  100                 105                 110
66 atg att tcc tgg atg tac ttg gtg ggc ttt tac agt ggc ata ttc ttt       563
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67 Met Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe
68           115                 120           125
70 gtc atg ctc atg agc att gat aga tac ctg gcg ata gtg cac gcg gtg    611
71 Val Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val
72          130              135              140
74 ttt tcc ttg agg gca agg acc ttg act tat ggg gtc atc acc agt ttg    659
75 Phe Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu
76      145              150              155
78 gct aca tgg tca gtg gct gtg ttc gcc tcc ctt cct ggc ttt ctg ttc    707
79 Ala Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe
80 160              165              170              175
82 agc act tgt tat act gag cgc aac cat acc tac tgc aaa acc aag tac    755
83 Ser Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr
84              180              185              190
86 tct ctc aac tcc acg acg tgg aag gtt ctc agc tcc ctg gaa atc aac    803
87 Ser Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn
88          195              200              205
90 att ctc gga ttg gtg atc ccc tta ggg atc atg ctg ttt tgc tac tcc    851
91 Ile Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser
92          210              215              220
94 atg atc atc agg acc ttg cag cat tgt aaa aat gag aag aag aac aag    899
95 Met Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys
96    225              230              235
98 gcg gtg aag atg atc ttt gcc gtg gtg gtc ctc ttc ctt ggg ttc tgg    947
99 Ala Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp
100 240              245              250              255
102 aca cct tac aac ata gtg ctc ttc cta gag acc ctg gtg gag cta gaa    995
103 Thr Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu
104          260              265              270
106 gtc ctt cag gac tgc acc ttt gaa aga tac ttg gac tat gcc atc cag   1043
107 Val Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln
108          275              280              285
110 gcc aca gaa act ctg gct ttt gtt cac tgc tgc ctt aat ccc atc atc   1091
111 Ala Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile
112          290              295              300
114 tac ttt ttt ctg ggg gag aaa ttt cgc aag tac atc cta cag ctc ttc   1139
115 Tyr Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe
116 305              310              315
118 aaa acc tgc agg ggc ctt ttt gtg ctc tgc caa tac tgt ggg ctc ctc   1187
119 Lys Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu
120 320              325              330              335
122 caa att tac tct gct gac acc ccc agc tca tct tac acg cag tcc acc   1235
123 Gln Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr
124          340              345              350
126 atg gat cat gat ctt cat gat gct ctg tag'gaaaaatgaa atggtgaaat    1285
127 Met Asp His Asp Leu His Asp Ala Leu  *
128          355              360
130 gcagagtcaa tgaactttc cacattcaga gcttacttta aaattggtat ttttaggtaa  1345
131 gagatccctg agccagtgtc aggaggaagg cttacaccca cagtggaaag acagcttctc  1405
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132 atcctgcagg cagctttttc tctcccacta gacaagtcca gcctggcaag ggttcacctg   1465
133 ggctgaggca tccttcctca caccaggctt gcctgcaggc atgagtcagt ctgatgagaa   1525
134 ctctgagcag tgcttgaatg aagttgtagg taatattgca aggcaaagac tattcccttc   1585
135 taacctgaac tgatgggttt ctccagaggg aattgcagag tactggctga tggagtaaat   1645
136 cgctaccttt tgctgtggca aatgggcccc cg                                 1677
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 360
140 <212> TYPE: PRT
141 <213> ORGANISM: H. sapiens
143 <400> SEQUENCE: 2
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144 Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
145  1               5                  10                  15
146 Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
147              20                  25                  30
148 Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
149          35                  40                  45
150 Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
151      50                  55                  60
152 Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
153 65                  70                  75                  80
154 Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
155                  85                  90                  95
156 Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
157              100                 105                 110
158 Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
159          115                 120                 125
160 Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
161      130                 135                 140
162 Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
163 145                 150                 155                 160
164 Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
165              165                 170                 175
166 Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
167              180                 185                 190
168 Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
169              195                 200                 205
170 Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
171      210                 215                 220
172 Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
173 225                 230                 235                 240
174 Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr
175              245                 250                 255
176 Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
177              260                 265                 270
178 Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
179              275                 280                 285
180 Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
181      290                 295                 300
182 Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys
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183 305                   310              315              320
184 Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
185               325                  330              335
186 Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met
187           340              345              350
188 Asp His Asp Leu His Asp Ala Leu
189           355              360
191 <210> SEQ ID NO: 3
192 <211> LENGTH: 538
193 <212> TYPE: DNA
194 <213> ORGANISM: H. sapiens
196 <220> FEATURE:
197 <221> NAME/KEY: CDS
198 <222> LOCATION: (53)...(337)
199 <223> OTHER INFORMATION: Coding sequence for TARC chemokine
201 <400> SEQUENCE: 3
202 ccctgagcag agggacctgc acacagagac tccctcctgg gctcctggca cc atg gcc    58
                                                              Met Ala
203                                                            1
204
206 cca ctg aag atg ctg gcc ctg gtc acc ctc ctc ctg ggg gct tct ctg   106
207 Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala Ser Leu
208         5                10                15
210 cag cac atc cac gca gct cga ggg acc aat gtg ggc cgg gag tgc tgc   154
211 Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys
212     20                  25                30
214 ctg gag tac ttc aag gga gcc att ccc ctt aga aag ctg aag acg tgg   202
215 Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys Thr Trp
216 35                  40                45                50
218 tac cag aca tct gag gac tgc tcc agg gat gcc atc gtt ttt gta act   250
219 Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr
220             55                  60                65
222 gtg cag ggc agg gcc atc tgt tcg gac ccc aac aac aag aga gtg aag   298
223 Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys
224         70                  75                80
226 aat gca gtt aaa tac ctg caa agc ctt gag agg tct tga agcctcctca    347
227 Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser  *
228         85                  90
230 ccccagactc ctgactgtct cccgggacta cctgggacct ccaccgttgg tgttcaccgc   407
231 ccccaccctg agcgcctggg tccaggggag gccttccagg gacgaagaag agccacagtg   467
232 agggagatcc catccccttg tctgaactgg agccatgggc acaaagggcc cagattaaag   527
233 tctttatcct c                                                         538
235 <210> SEQ ID NO: 4
236 <211> LENGTH: 94
237 <212> TYPE: PRT
238 <213> ORGANISM: H. sapiens
240 <400> SEQUENCE: 4
241 Met Ala Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala
242 1               5                10                15
243 Ser Leu Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu
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244                20              25              30
245 Cys Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys
246            35              40              45
247 Thr Trp Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe
248    50              55              60
249 Val Thr Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg
250 65              70              75              80
251 Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
252            85              90

254 <210> SEQ ID NO: 5
255 <211> LENGTH: 2923
256 <212> TYPE: DNA
257 <213> ORGANISM: H. sapiens
259 <220> FEATURE:
260 <221> NAME/KEY: CDS
261 <222> LOCATION: (20)...(301)
262 <223> OTHER INFORMATION: Coding sequence for MDC chemokine
264 <400> SEQUENCE: 5
265 gagacataca ggacagagc atg gct cgc cta cag act gca ctc ctg gtt gtc        52
266                    Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val
267                     1               5              10
269 ctc gtc ctc ctt gct gtg gcg ctt caa gca act gag gca ggc ccc tac       100
270 Leu Val Leu Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr
271            15              20              25
273 ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac       148
274 Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr
275            30              35              40
277 cgt ctg ccc ctg cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc       196
278 Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser
279    45              50              55
281 tgc ccg agg cct ggc gtg gtg ttg cta acc ttc agg gat aag gag atc       244
282 Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile
283 60              65              70              75
285 tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg       292
286 Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu
287            80              85              90
289 agc caa tga agagcctact ctgatgaccg tggccttggc tcctccagga             341
290 Ser Gln  *
293 aggctcagga gccctacctc cctgccatta tagctgctcc ccgccagaag cctgtgccaa     401
294 ctctctgcat tccctgatct ccatccctgt ggctgtcacc cttggtcacc tccgtgctgt     461
295 cactgccatc tcccccctga ccctctaac ccatcctctg cctccctccc tgcagtcaga      521
296 gggtcctgtt cccatcagcg attcccctgc ttaaaccctt ccatgactcc ccactgccct     581
297 aagctgaggt cagtctccca agcctggcat gtggcccct ggatctgggt tccatctctg      641
298 tctccagcct gcccacttcc cttcatgaat gttgggtatgt tgctgacact cagaaagtcc    701
299 catactacac atcccacttc tgggtctttg cctgggatgt tgctgacact cagaaagtcc     761
300 caccacctgc acatgtgtag ccccaccagc cctccaaggc attgctcgcc caagcagctg     821
301 gtaattccat ttcatgtatt agatgtcccc tggccctctg tccctctta ataaccctag      881
302 tcacagtctc cgcagattct tgggatttgg gggtttctc ccccacctct ccactagttg      941
303 gaccaaggtt ctagctaag ttactctagt ctccaagcct ctagcataga gcactgcaga     1001
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/837,446

DATE: 05/07/2001
TIME: 17:55:06

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05072001\I837446.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number